1632

1632

```
      RAW SEQUENCE LISTING              DATE: 02/06/2002
      PATENT APPLICATION:  US/09/721,904A   TIME: 09:38:08

      Input Set : A:\seqlist.asc.txt
      Output Set: N:\CRF3\02062002\I721904A.raw
```

P.5

ENTERED

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 3 <110> APPLICANT: JULIUS, Michael H.
 4        FILIPP, Dominik
 6 <120> TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
 7        LAIT/sCD14-PROTEIN
 9 <130> FILE REFERENCE: 47841/00063
11 <140> CURRENT APPLICATION NUMBER: US 09/721,904A
12 <141> CURRENT FILING DATE: 2000-11-27
14 <150> PRIOR APPLICATION NUMBER: PCT/CA99/00482
15 <151> PRIOR FILING DATE: 1999-05-27
17 <150> PRIOR APPLICATION NUMBER: US 60/086,884
18 <151> PRIOR FILING DATE: 1998-05-27
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: Wordperfect 9.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1122
26 <212> TYPE: DNA
27 <213> ORGANISM: bovine
29 <400> SEQUENCE: 1
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32 gacacaacag aaccctgcga gctggacgac gacgatttcc gttgtgtctg caacttcacg     120
34 gatccgaagc ctgactggtc tagcgccgtt cagtgtatgg ttgccgtcga ggtggagatc     180
36 agtgccggcg gccgcagcct ggaacagttt ctcaagggag ccgacaccaa cccgaagcag     240
38 tatgctgaca caatcaaggc tctgcgcgtt cggcgactca agctgggcgc tgcacaggtt     300
40 cctgctcagc ttctggtcgc cgttctgcgc gcgctcgggt actctcgtct caaggaactg     360
42 acgcttgagg acctggaggt aaccggccca acgcccccga cgcctctgga agccgctggg     420
44 cctgcgctca ccaccctcag tctgcgtaac gtatcgtgga aacaggagg tgcctggctc      480
46 ggcgaactgc agcagtggct caagcctggg ctcagggtgc tgaacattgc ccaagcacac     540
48 tcgcttgcct ttccgtgcgc agggctctcc accttcgagg cgctcaccac cctagacctg     600
50 tctgacaatc ccagtctcgg cgacacgggg ctgatggcag ctctctgtcc gaacaagttc     660
52 ccggccctcc aatatctagc gctacgcaac gcggggatgg agacgccgag cggcgtgtgc     720
54 gcggcgctgg cggcagcgag ggtgcagccc caaagcctgg acctcagcca caactcgctg     780
56 cgcgtcaccg ccccgggtgc tacccgatgt gtctggccca gtgcactaag gtctctcaat     840
58 ttgtcgttcg ctgggctgga gcaagtgcct aagggactgc ccctaagct cagcgtgctt      900
60 gatctcagct gcaacaagct aagcagggag ccgcggcgag acgagctgcc cgaggtaaat     960
62 gacctgactc tggacggaaa tccctttctg gaccctggag ccctccagca ccaaaatgac    1020
64 ccgatgatct ccggcgtggt cccagcctgt gcgcgttctg ccttgaccat ggggggtgtca   1080
66 ggagccctgg cgctgcttca aggagcccga ggcttcgcgt aa                       1122
69 <210> SEQ ID NO: 2
70 <211> LENGTH: 1128
71 <212> TYPE: DNA
72 <213> ORGANISM: human
74 <400> SEQUENCE: 2
75 atggagcgcg cgtcctgctt gttgctgctg ctgctgccgc tggtgcacgt ctctgcgacc     60
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RAW SEQUENCE LISTING   DATE: 02/06/2002
PATENT APPLICATION: US/09/721,904A TIME: 09:38:08

Input Set : A:\seqlist.asc.txt
Output Set: N:\CRF3\02062002\I721904A.raw

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 77 acgccagaac cttgtgagct ggacgatgaa gatttccgct gcgtctgcaa cttctccgaa       120
 79 cctcagcccg actggtccga agccttccag tgtgtgtctg cagtagaggt ggagatccat       180
 81 gccggcggtc tcaacctaga gccgtttcta aagcgcgtcg atgcggacgc cgacccgcgg       240
 83 cagtatgctg acacggtcaa ggctctccgc gtgcggcggc tcacagtggg agccgcacag       300
 85 gttcctgctc agctactggt aggcgccctg cgtgtgctag cgtactcccg cctcaaggaa       360
 87 ctgacgctcg aggacctaaa gataaccggc accatgcctc cgctgcctct ggaagccaca       420
 89 ggacttgcac tttccagctt gcgcctacgc aacgtgtcgt gggcgacagg gcgttcttgg       480
 91 ctcgccgagc tgcagcagtg gctcaagcca ggcctcaagg tactgagcat tgcccaagca       540
 93 cactcgcctg ccttttcctg cgaacaggtt cgcgccttcc cggcccttac cagcctagac       600
 95 ctgtctgaca atcctggact gggcgaacgc ggactgatgg cggctctctg tccccacaag       660
 97 ttcccggcca tccagaatct agcgctgcgc aacacaggaa tggagacgcc.cacaggcgtg       720
 99 tgcgccgcac tggcggcggc aggtgtgcag ccccacagcc tagacctcag ccacaactcg       780
101 ctgcgcgcca ccgtaaaccc tagcgctccg agatgcatgt ggtccagcgc cctgaactcc       840
103 ctcaatctgt cgttcgctgg gctggaacag gtgcctaaag gactgccagc caagctcaga       900
105 gtgctcgatc tcagctgcaa cagactgaac agggcgccgc agcctgacga gctgcccgag       960
107 gtggataacc tgacactgga cgggaatccc ttcctggtcc ctggaactgc cctcccccac      1020
109 gagggctcaa tgaactccgg cgtggtccca gcctgtgcac gttcgaccct gtcggtgggg      1080
111 gtgtcgggaa ccctggtgct gctccaaggg gcccggggct ttgcctaa                  1128
114 <210> SEQ ID NO: 3
115 <211> LENGTH: 1101
116 <212> TYPE: DNA
117 <213> ORGANISM: murine
119 <400> SEQUENCE: 3
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C-->120 atggagcgtg tgcttggctt gttgctgttg cttctggtgc acgcctctcc cgccccacca        60
122 gagccctgcg agctagacga ggaaagttgt tcctgcaact tctcagatcc gaagccagat       120
124 tggtccagcg ctttcaattg tttgggggcg gcagatgtgg aattgtacgg cggcggccgc       180
126 agcctggaat accttctaaa gcgtgtggac acggaagcag atctggggca gttcactgat       240
128 attatcaagt ctctgtcctt aaagcggctt acggtgcggg ccgcgcggat tcctagtcgg       300
130 attctattcg gagccctgcg tgtgctcggg atttccggcc tccaggaact gactcttgaa       360
132 aatctcgagg taaccggcac cgcgccgcca ccgcttctgg aagccaccgg acccgatctc       420
134 aacatcttga acctccgcaa cgtgtcgtgg gcaacaaggg atgcctggct cgcagaactg       480
136 cagcagtggc taaagcctgg actcaaggta ctgagtattg cccaagcaca ctcactcaac       540
138 tttcctgcg aacaggtccg cgtcttccct gccctctcca ccttagacct gtctgacaat       600
140 cctgaattgg gcgagagagg actgatctca gccctctgtc ccctcaagtt cccgaccctc       660
142 caagtttttag cgctgcgtaa cgcgggggatg gagacgccca gcggcgtgtg ctctgcgctg       720
144 gccgcagcaa gggtacagct gcaaggacta gaccttagtc acaattcact gcgggatgct       780
146 gcaggcgctc cgagttgtga ctggcccagt cagctaaact cgctcaatct gtctttcact       840
148 gggctgaagc aggtacctaa agggctgcca gccaagctca gcgtgctgga tctcagttac       900
150 aacaggctgg ataggaaccc tagcccagat gagctgcccc aagtggggaa cctgtcactt       960
152 aaaggaaatc ccttttttgga ctctgaatcc cactcggaga agtttaactc tggcgtagtc      1020
154 accgccggag ctccatcatc ccaagcagtg gccttgtcag gaactctggc tttgctccta      1080
156 ggagatcgcc tctttgttta a                                                1101
159 <210> SEQ ID NO: 4
160 <211> LENGTH: 373
161 <212> TYPE: PRT
162 <213> ORGANISM: bovine
164 <400> SEQUENCE: 4
165 Met Val Cys Val Pro Tyr Leu Leu Leu Leu Leu Pro Ser Leu Leu
166 1            5                 10              15
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/721,904A

DATE: 02/06/2002
TIME: 09:38:08

Input Set : A:\seqlist.asc.txt
Output Set: N:\CRF3\02062002\I721904A.raw

```
168 Arg Val Ser Ala Asp Thr Thr Glu Pro Cys Glu Leu Asp Asp Asp Asp
169         20              25              30
171 Phe Arg Cys Val Cys Asn Phe Thr Asp Pro Lys Pro Asp Trp Ser Ser
172         35              40              45
174 Ala Val Gln Cys Met Val Ala Val Glu Val Glu Ile Ser Ala Gly Gly
175         50              55              60
177 Arg Ser Leu Glu Gln Phe Leu Lys Gly Ala Asp Thr Asn Pro Lys Gln
178 65              70              75              80
180 Tyr Ala Asp Thr Ile Lys Ala Leu Arg Val Arg Arg Leu Lys Leu Gly
181             85              90              95
183 Ala Ala Gln Val Pro Ala Gln Leu Leu Val Ala Val Leu Arg Ala Leu
184         100             105             110
186 Gly Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Glu Val Thr
187         115             120             125
189 Gly Pro Thr Pro Pro Thr Pro Leu Glu Ala Ala Gly Pro Ala Leu Thr
190     130             135             140
192 Thr Leu Ser Leu Arg Asn Val Ser Trp Thr Thr Gly Gly Ala Trp Leu
193 145             150             155             160
195 Gly Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Arg Val Leu Asn Ile
196             165             170             175
198 Ala Gln Ala His Ser Leu Ala Phe Pro Cys Ala Gly Leu Ser Thr Phe
199         180             185             190
201 Glu Ala Leu Thr Thr Leu Asp Leu Ser Asp Asn Pro Ser Leu Gly Asp
202         195             200             205
204 Thr Gly Leu Met Ala Ala Leu Cys Pro Asn Lys Phe Pro Ala Leu Gln
205     210             215             220
207 Tyr Leu Ala Leu Arg Asn Ala Gly Met Glu Thr Pro Ser Gly Val Cys
208 225             230             235             240
210 Ala Ala Leu Ala Ala Ala Arg Val Gln Pro Gln Ser Leu Asp Leu Ser
211             245             250             255
213 His Asn Ser Leu Arg Val Thr Ala Pro Gly Ala Thr Arg Cys Val Trp
214             260             265             270
216 Pro Ser Ala Leu Arg Ser Leu Asn Leu Ser Phe Ala Gly Leu Glu Gln
217         275             280             285
219 Val Pro Lys Gly Leu Pro Pro Lys Leu Ser Val Leu Asp Leu Ser Cys
220     290             295             300
222 Asn Lys Leu Ser Arg Glu Pro Arg Arg Asp Glu Leu Pro Glu Val Asn
223 305             310             315             320
225 Asp Leu Thr Leu Asp Gly Asn Pro Phe Leu Asp Pro Gly Ala Leu Gln
226             325             330             335
228 His Gln Asn Asp Pro Met Ile Ser Gly Val Val Pro Ala Cys Ala Arg
229         340             345             350
231 Ser Ala Leu Thr Met Gly Val Ser Gly Ala Leu Ala Leu Leu Gln Gly
232         355             360             365
234 Ala Arg Gly Phe Ala
235     370
238 <210> SEQ ID NO: 5
239 <211> LENGTH: 375
240 <212> TYPE: PRT
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RAW SEQUENCE LISTING   DATE: 02/06/2002
PATENT APPLICATION: US/09/721,904A   TIME: 09:38:08

Input Set : A:\seqlist.asc.txt
Output Set: N:\CRF3\02062002\I721904A.raw

```
241 <213> ORGANISM: human
243 <400> SEQUENCE: 5
244 Met Glu Arg Ala Ser Cys Leu Leu Leu Leu Leu Leu Pro Leu Val His
245 1               5                   10                  15
247 Val Ser Ala Thr Thr Pro Glu Pro Cys Glu Leu Asp Asp Glu Asp Phe
248             20                  25                  30
250 Arg Cys Val Cys Asn Phe Ser Glu Pro Gln Pro Asp Trp Ser Glu Ala
251         35                  40                  45
253 Phe Gln Cys Val Ser Ala Val Glu Val Glu Ile His Ala Gly Gly Leu
254     50                  55                  60
256 Asn Leu Glu Pro Phe Leu Lys Arg Val Asp Ala Asp Ala Asp Pro Arg
257 65                  70                  75                  80
259 Gln Tyr Ala Asp Thr Val Lys Ala Leu Arg Val Arg Arg Leu Thr Val
260             85                  90                  95
262 Gly Ala Ala Gln Val Pro Ala Gln Leu Leu Val Gly Ala Leu Arg Val
263             100                 105                 110
265 Leu Ala Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Lys Ile
266         115                 120                 125
268 Thr Gly Thr Met Pro Pro Leu Pro Leu Glu Ala Thr Gly Leu Ala Leu
269     130                 135                 140
271 Ser Ser Leu Arg Leu Arg Asn Val Ser Trp Ala Thr Gly Arg Ser Trp
272 145                 150                 155                 160
274 Leu Ala Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Lys Val Leu Ser
275             165                 170                 175
277 Ile Ala Gln Ala His Ser Pro Ala Phe Ser Tyr Glu Gln Val Arg Ala
278             180                 185                 190
280 Phe Pro Ala Leu Thr Ser Leu Asp Leu Ser Asp Asn Pro Gly Leu Gly
281         195                 200                 205
283 Glu Arg Gly Leu Met Ala Ala Leu Cys Pro His Lys Phe Pro Ala Ile
284     210                 215                 220
286 Gln Asn Leu Ala Leu Arg Asn Thr Gly Met Glu Thr Pro Thr Gly Val
287 225                 230                 235                 240
289 Cys Ala Ala Leu Ala Ala Ala Gly Val Gln Pro His Ser Leu Asp Leu
290             245                 250                 255
292 Ser His Asn Ser Leu Arg Ala Thr Val Asn Pro Ser Ala Pro Arg Cys
293             260                 265                 270
295 Met Trp Ser Ser Ala Leu Asn Ser Leu Asn Leu Ser Phe Ala Gly Leu
296         275                 280                 285
298 Glu Gln Val Pro Lys Gly Leu Pro Ala Lys Leu Arg Val Leu Asp Leu
299     290                 295                 300
301 Ser Cys Asn Arg Leu Asn Arg Ala Pro Gln Pro Asp Glu Leu Pro Glu
302 305                 310                 315                 320
304 Val Asp Asn Leu Thr Leu Asp Gly Asn Pro Phe Leu Val Pro Gly Thr
305             325                 330                 335
307 Ala Leu Pro His Glu Gly Ser Met Asn Ser Gly Val Val Pro Ala Cys
308             340                 345                 350
310 Ala Arg Ser Thr Leu Ser Val Gly Val Ser Gly Thr Leu Val Leu Leu
311         355                 360                 365
313 Gln Gly Ala Arg Gly Phe Ala
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RAW SEQUENCE LISTING
· PATENT APPLICATION: US/09/721,904A

DATE: 02/06/2002
TIME: 09:38:08

Input Set : **A:\seqlist.asc.txt**
Output Set: **N:\CRF3\02062002\I721904A.raw**

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314      370                    375
317 <210> SEQ ID NO: 6
318 <211> LENGTH: 366
319 <212> TYPE: PRT
320 <213> ORGANISM: murine
322 <400> SEQUENCE: 6
323 Met Glu Arg Val Leu Gly Leu Leu Leu Leu Leu Val His Ala Ser
324 1               5                   10                  15
326 Pro Ala Pro Pro Glu Pro Cys Glu Leu Asp Glu Glu Ser Cys Ser Cys
327             20                  25                  30
329 Asn Phe Ser Asp Pro Lys Pro Asp Trp Ser Ser Ala Phe Asn Cys Leu
330         35                  40                  45
332 Gly Ala Ala Asp Val Glu Leu Tyr Gly Gly Gly Arg Ser Leu Glu Tyr
333     50                  55                  60
335 Leu Leu Lys Arg Val Asp Thr Glu Ala Asp Leu Gly Gln Phe Thr Asp
336 65                  70                  75                  80
338 Ile Ile Lys Ser Leu Ser Leu Lys Arg Leu Thr Val Arg Ala Ala Arg
339             85                  90                  95
341 Ile Pro Ser Arg Ile Leu Phe Gly Ala Leu Arg Val Leu Gly Ile Ser
342             100                 105                 110
344 Gly Leu Gln Glu Leu Thr Leu Glu Asn Leu Glu Val Thr Gly Thr Ala
345         115                 120                 125
347 Pro Pro Pro Leu Leu Glu Ala Thr Gly Pro Asp Leu Asn Ile Leu Asn
348     130                 135                 140
350 Leu Arg Asn Val Ser Trp Ala Thr Arg Asp Ala Trp Leu Ala Glu Leu
351 145                 150                 155                 160
353 Gln Gln Trp Leu Lys Pro Gly Leu Lys Val Leu Ser Ile Ala Gln Ala
354             165                 170                 175
356 His Ser Leu Asn Phe Ser Cys Glu Gln Val Arg Val Phe Pro Ala Leu
357         180                 185                 190
359 Ser Thr Leu Asp Leu Ser Asp Asn Pro Glu Leu Gly Glu Arg Gly Leu
360         195                 200                 205
362 Ile Ser Ala Leu Cys Pro Leu Lys Phe Pro Thr Leu Gln Val Leu Ala
363     210                 215                 220
365 Leu Arg Asn Ala Gly Met Glu Thr Pro Ser Gly Val Cys Ser Ala Leu
366 225                 230                 235                 240
368 Ala Ala Ala Arg Val Gln Leu Gln Gly Leu Asp Leu Ser His Asn Ser
369             245                 250                 255
371 Leu Arg Asp Ala Ala Gly Ala Pro Ser Cys Asp Trp Pro Ser Gln Leu
372             260                 265                 270
374 Asn Ser Leu Asn Leu Ser Phe Thr Gly Leu Lys Gln Val Pro Lys Gly
375         275                 280                 285
377 Leu Pro Ala Lys Leu Ser Val Leu Asp Leu Ser Tyr Asn Arg Leu Asp
378     290                 295                 300
380 Arg Asn Pro Ser Pro Asp Glu Leu Pro Gln Val Gly Asn Leu Ser Leu
381 305                 310                 315                 320
383 Lys Gly Asn Pro Phe Leu Asp Ser Glu Ser His Ser Glu Lys Phe Asn
384             325                 330                 335
386 Ser Gly Val Val Thr Ala Gly Ala Pro Ser Ser Gln Ala Val Ala Leu
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/721,904A

DATE: 02/06/2002
TIME: 09:38:09

Input Set : A:\seqlist.asc.txt
Output Set: N:\CRF3\02062002\I721904A.raw

L:120 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=3
L:414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7